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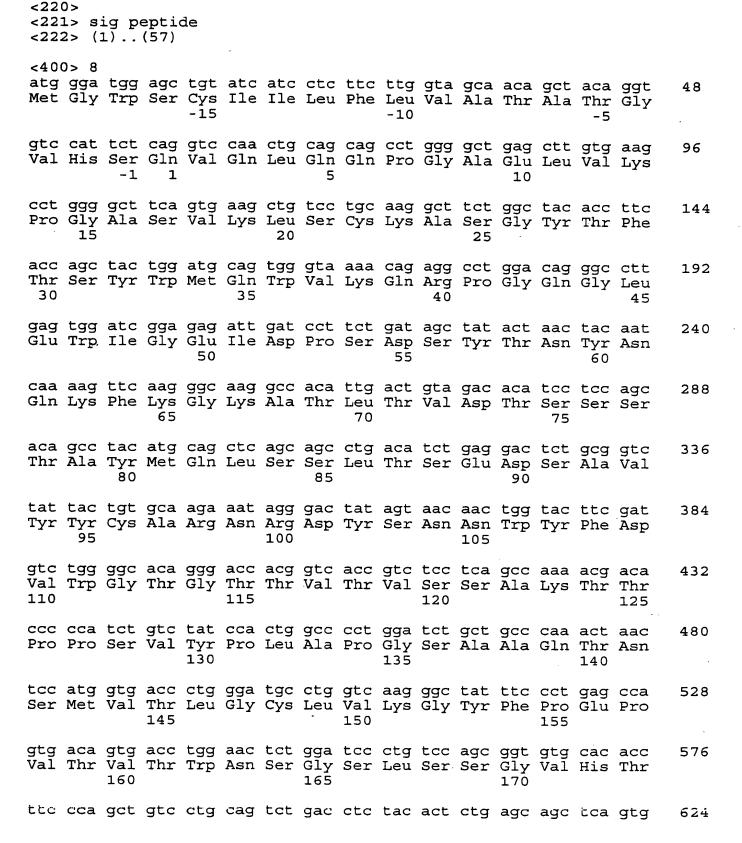
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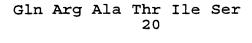
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chain kappa subtype 3

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Leu His His Asp

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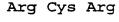
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His Cys Asp Pro



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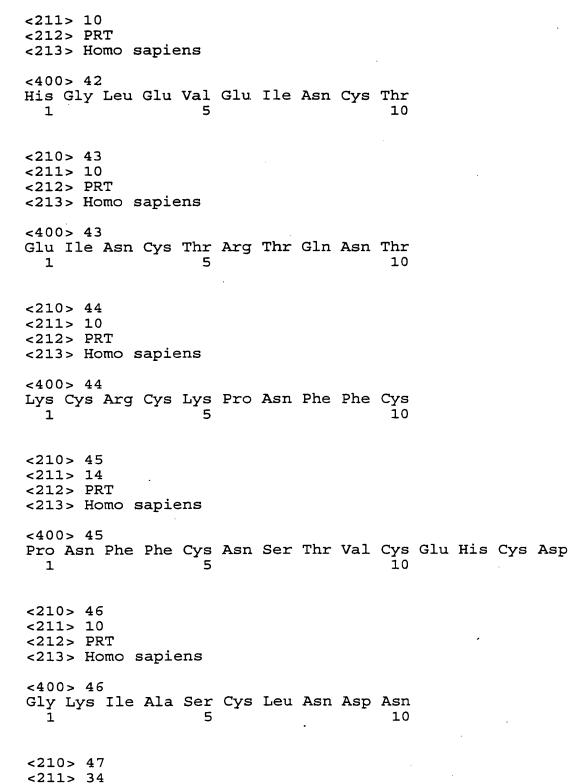
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att gtg ctc acc caa tct cca ggt act ttg tct ctg tct cca ggg gag Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu 5 10 15	150
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aaa Lys	gtc Val 195	tac Tyr	gcc Ala	tgc Cys	gaa Glu	gtc Val 200	acc Thr	cat His	cag Gln	ggc Gly	ctg Leu 205	agc Ser	tcg Ser	ccc Pro	gtc. Val	726
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Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 30 35 40

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 45 50 55 60

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
65 70 75

Leu Thr Ile Ser Arg Leu Glu Pro Ala Asp Phe Ala Val Tyr Tyr Cys 80 85 90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Arg Leu 95 100 105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 125 130 135 140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 145 150 155

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 160 165 170

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 175 180 185

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<211> 768





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														cat His 80		342
														aat Asn		390





gat c Asp P	cct Pro	cgg Arg 100	acg Thr	ttc Phe	ggt Gly	caa Gln	ggc Gly 105	acc Thr	agg Arg	ctg Leu	gaa Glu	atc Ile 110	aaa Lys	cgg Arg	act Thr	438
gtg g Val A	gct Ala L15	gca Ala	cca Pro	tct Ser	gtc Val	ttc Phe 120	atc Ile	ttc Phe	ccg Pro	cca Pro	tct Ser 125	gat Asp	gag Glu	cag Gln	ttg Leu	486
aaa t Lys S 130	ct Ser	gga Gly	act Thr	gcc Ala	tct Ser 135	gtt Val	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	534
aga g Arg G	gag Slu	gcc Ala	aaa Lys	gta Val 150	cag Gln	tgg Trp	aaa Lys	gtg Val	gat Asp 155	aac Asn	gcc Ala	ctc Leu	caa Gln	tcg Ser 160	ggt Gly	582
aac t Asn S	cc Ser	cag Gln	gag Glu 165	agt Ser	gtc Val	aca Thr	gag Glu	cag Gln 170	gac Asp	agc Ser	aag Lys	gac Asp	agc Ser 175	acc Thr	tac Tyr	630
agc c Ser L	ctc Leu	agc Ser 180	agc Ser	acc Thr	ctg Leu	acg Thr	ctg Leu 185	agc Ser	aaa Lys	gca Ala	gac Asp	tac Tyr 190	gag Glu	aaa Lys	cac His	678
aaa g Lys V 1	gtc Val 195	tac Tyr	gcc Ala	tgc Cys	gaa Glu	gtc Val 200	acc Thr	cat His	cag Gln	ggc Gly	ctg Leu 205	agc Ser	tcg Ser	ccc Pro	gtc Val	726
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<211> 238

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<213> Artificial Sequence

<220>

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-1 1 5 10

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 30 35 40





Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 125 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 145 150 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 165 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 180 175 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 210 205

<210> 53

<211> 768

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (40)..(753)

<220>

<221> mat peptide

<222> (100)...(753)

<220>

<221> sig peptide

<222> (40)..(99)

<220>

<223> Description of Artificial Sequence: Designed DNA encoding the light chain of humanized anti-human





Fas antibody

<pre><400> 53 cccaagctta agaagcatcc tctcatctag ttctcagag atg gag aca gac aca</pre>														54		
atc o Ile I -15																102
att g Ile V	gtg Val	ctc Leu	acc Thr 5	caa Gln	tct Ser	cca Pro	ggt Gly	act Thr 10	ttg Leu	tct Ser	ctg Leu	tct Ser	cca Pro 15	ggg Gly	gag Glu	150
agg g Arg A																198
gat a Asp s																246
ctc o Leu I 50																294
ttt a Phe S	agt Ser	ggc Gly	agt Ser	ggg Gly 70	tct Ser	gly aaa	aca Thr	gac Asp	ttc Phe 75	acc Thr	ctc Leu	acc Thr	atc Ile	cat His 80	cct Pro	342
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gat o Asp I	cct Pro	cgg Arg 100	acg Thr	ttc Phe	ggt Gly	caa Gln	ggc Gly 105	acc Thr	agg Arg	ctg Leu	gaa Glu	atc Ile 110	aaa Lys	cgg Arg	act Thr	438
gtg g Val A																486
aaa t Lys S 130	tct Ser	gga Gly	act Thr	gcc Ala	tct Ser 135	gtt Val	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	534
aga g Arg (gag Glu	gcc Ala	aaa Lys	gta Val 150	cag Gln	tgg Trp	aaa Lys	gtg Val	gat Asp 155	aac Asn	gcc Ala	ctc Leu	caa Gln	tcg Ser 160	ggt Gly	582
aac t Asn S																630







agc ctc agc agc acc ctg acg ct	tg agc aaa gca gac	tac gag aaa cac 678
Ser Leu Ser Ser Thr Leu Thr Le	eu Ser Lys Ala Asp	Tyr Glu Lys His
180	85	190

aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc 726 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val 195 200 205

aca aag agc ttc aac agg gga gag tgt tagtaagaat tcggg 768 Thr Lys Ser Phe Asn Arg Gly Glu Cys 210

<210> 54

<211> 238 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 54

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 45

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

Leu Thr Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Arg Leu 95 100

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 125 130 135





ASN AS	sn Pne	Tyr	145	Arg	GIU	Ата	гÀз	150	GIN	Trp	гÀг	vaı	155	Asn	
Ala Le	eu Gln	Ser 160	Gly	Asn	Ser	Gln	Glu 165	Ser	Val	Thr	Glu	Gln 170	Asp	Ser	
Lys As	sp Ser 175	Thr	Tyr	Ser	Leu	Ser 180	Ser	Thr	Leu	Thr	Leu 185	Ser	Lys	Ala	
Asp Ty	r Glu 90	Lys	His	Lys	Val 195	Tyr	Ala	Cys	Glu	Val 200	Thr	His	Gln	Gly	
Leu Se 205	er Ser	Pro	Val	Thr 210	Lys	Ser	Phe	Asn	Arg 215	Gly	Glu	Cys			
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<210><211><212><213>	44	icia	l Sed	quen	ce										
<220> <223>	Descriampli:	fy a	frag	gment	t of	DNA	ence	oding	g the			r to			





<400> ccaggt	57 actt tgtctctgtc tccaggggag agggccaccc tctc	44
<210><211><211><212><213>	44	
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<210><211><211><212><213>	45	
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<210><211><211><212><213>	52	
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<210><211><211><212><213>	58	
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chain of humanized anti-Fas antibody

<400> 61 ctcgtctgga gccggcggat tttgcagtct attactgtca gcaaagtaat gaggatcc	58
<210> 62 <211> 55 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody	
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<210> 63 <211> 55 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody	
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<210> 64 <211> 45 <212> DNA <213> Artificial Sequence	
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<223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody	
<400>	65	
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<211>		
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3 3		
010		
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<223>	Description of Artificial Sequence: Sequencing primer for DNAs encoding the light chains of humanized anti-Fas antibodies	
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<210><211><212>	20	







<220>

<223> Description of Artificial Sequence: Sequencing primer for DNAs encoding the light chains of humanized anti-Fas antibodies

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<210> 74

<211> 457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding the partial peptide of the heavy chain of a humanized anti-Fas antibody

<220>

<221> CDS

<222> (21)..(455)

<220>

<221> mat peptide

<222> (78)..(455)

<220>

<221> sig peptide

<222> (21)..(77)

<400> 74

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Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly
-5 -1 1 5

gct gag gtc aag aag cct ggg gct tca gtg aag gtg tcc tgc aag gct 149 Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala 10 15 20

tct ggc tac acc ttc acc agc tac tgg atg cag tgg gta aaa cag gcc 197 Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Ala 25 30 35 40

cct gga cag agg ctt gag tgg atg gga gag att gat cct tct gat agc 245
Pro Gly Gln Arg Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser
45 50 55





								2	79							
	act Thr															293
gac Asp	aca Thr	tcc Ser 75	gct Ala	agc Ser	aca Thr	gcc Ala	tac Tyr 80	atg Met	gag Glu	ctc Leu	agc Ser	agc Ser 85	ctg Leu	aga Arg	tct Ser	341
	gac Asp 90															389
	tgg Trp															437
	gcc Ala					cc									·	457
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Val	His	Ser -1	Gln 1	Val	Gln	Leu	Val 5	Gln	Ser	Gly	Ala	Glu 10	Val	Lys	Lys	
Pro	Gly 15	Ala	Ser	Val	Lys	Val 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Tyr	Thr	Phe	
Thr 30	Ser	Tyr	Trp	Met	Gln 35	Trp	Val	Lys	Gln	Ala 40	Pro	Gly	Gln	Arg	Leu 45	

Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn 50 . Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ala Ser 70 .

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 80 85 90

<400> 78



Tyr	Tyr 95	Cys	Ala	Arg	Asn	Arg 100	Asp	Tyr	Ser	Asn	Asn 105	Trp	Tyr	Phe	Asp	
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Gly																
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)> 76 agct	-	gctto	gacct	c a	ccat	gggat	gga	agcto	gtat						40
<211 <212)> 75 L> 48 2> DI 3> A1	3 NA	icial	l Sed	quenc	ce										·
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<220>





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<210><211><212><213>	50	
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<210><211><211><212><213>	44	





<223>	Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding variable region in the heavy chain of a humanized anti-Fas antibody	
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<210><211><212><212><213>	55	
<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding variable region in the heavy chain of a humanized anti-Fas antibody	
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<210><211><211><212><213>	39	
<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain	
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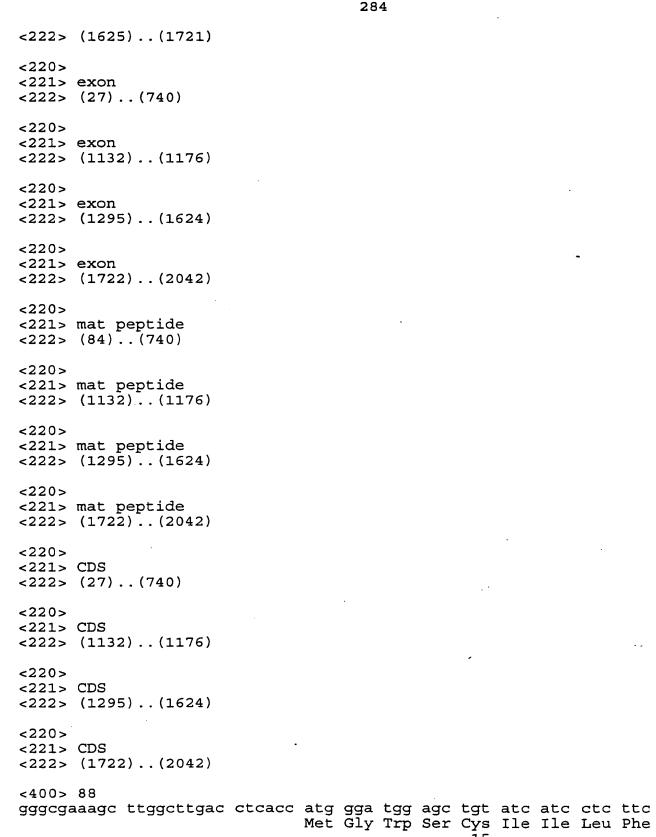
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<220>

<221> intron

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      constant region of human immunoglobulin G1 heavy
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<222> (27)..(83)
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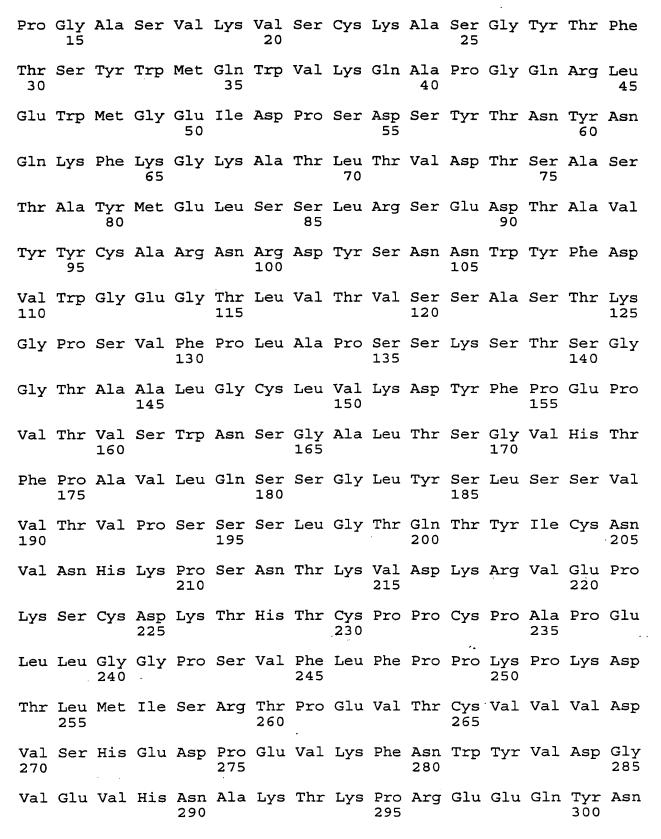
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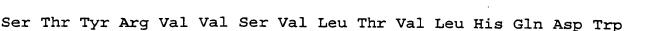
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
-1 1 5 10









Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro 320 325 330

310

289

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 335 340 345

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 350 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lŷs Thr 385 390 395

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 400 405 410

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 415 420 425

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 430 435 440 445

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

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20

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<223> Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

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<400> gttttg	,	20
<210><211><212>	94 ggggg gaagaggaag 95 20	20





humanized anti-Fas antibody

<400> 95 ccagtcctgg tgcaggacgg	20
<210> 96 <211> 20 <212> DNA <213> Artificial Sequence	
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<223>	Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody	
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att Ile	gtg Val	ctc Leu	acc Thr 5	caa Gln	tct Ser	cca Pro	ggt Gly	act Thr 10	ttg Leu	tct Ser	ctg Leu	tct Ser	cca Pro 15	Gly ggg	gag Glu	150
agg Arg	gcc Ala	acc Thr 20	ctc Leu	tcc Ser	tgc Cys	aag Lys	gcc Ala 25	agc Ser	caa Gln	agt Ser	gtt Val	gat Asp 30	tat Tyr	gat Asp	ggt Gly	198
gat Asp	agt Ser 35	tat Tyr	atg Met	aac Asn	tgg Trp	tac Tyr 40	caa Gln	cag Gln	aaa Lys	cca Pro	gga Gly 45	cag Gln	gca Ala	ccc Pro	aga Arg	246
ctc Leu 50	ctc Leu	atc Ile	tat Tyr	gct Ala	gca Ala 55	tcc Ser	aat Asn	ctc Leu	gaa Glu	tct Ser 60	gly aaa	atc Ile	cca Pro	gac Asp	agg Arg 65	294
ttt Phe	agt Ser	ggc Gly	agt Ser	ggg Gly 70	tct Ser	gly gag	aca Thr	gac Asp	ttc Phe 75	acc Thr	ctc Leu	acc Thr	atc Ile	tct Ser 80	cgt Arg	342
ctg Leu	gag Glu	ccg Pro	gag Glu 85	gat Asp	ttt Phe	gca Ala	gtc Val	tat Tyr 90	tac Tyr	tgt Cys	cag Gln	caa Gln	agt Ser 95	aat Asn	gag Glu	390
gat Asp	cct Pro	cgg Arg 100	acg Thr	ttc Phe	ggt Gly	caa Gln	ggc Gly 105	acc Thr	aag Lys	ctg Leu	gaa Glu	atc Ile 110	aaa Lys	cgg Arg	act Thr	438
gtg Val	gct Ala 115	gca Ala	cca Pro	tct Ser	gtc Val	ttc Phe 120	atc Ile	ttc Phe	ccg Pro	cca Pro	tct Ser 125	gat Asp	gag Glu	cag Gln	ttg Leu	486
aaa Lys 130	tct Ser	gga Gly	act Thr	gcc Ala	tct Ser 135	gtt Val	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	534
														tcg Ser 160		582
aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	630

110





								2	95							
Asn	Ser	Gln	Glu 165	Ser	Val	Thr	Glu	Gln 170	Asp	Ser	Lys	Asp	Ser 175	Thr	Tyr	
agc Ser	ctc Leu	agc Ser 180	agc Ser	acc Thr	ctg Leu	acg Thr	ctg Leu 185	agc Ser	aaa Lys	gca Ala	gac Asp	tac Tyr 190	gag Glu	aaa Lys	cac His	678
aaa Lys	gtc Val 195	tac Tyr	gcc Ala	tgc Cys	gaa Glu	gtc Val 200	acc Thr	cat His	cag Gln	ggc Gly	ctg Leu 205	agc Ser	tcg Ser	ccc Pro	gtc Val	726
	aag Lys								tagt	aaga	aat t	cggg				768
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	0> 10 Glu		Asp	Thr	Ile -15	Leu	Leu	Trp	Val	Leu -10	Leu	Leu	Trp	Val	Pro -5	
Gly	Ser	Thr	Gly -1	Glu 1	Ile	Val	Leu	Thr 5	Gln	Ser	Pro	Gly	Thr 10	Leu	Ser	
Leu	Ser	Pro 15	Gly	Glu	Arg	Ala	Thr 20	Leu	Ser	Cys	Lys	Ala 25	Ser	Gln	Ser	
Val	Asp 30	Tyr	Asp	Gly	Asp	Ser 35	Tyr	Met	Asn	Trp	Tyr 40	Gln	Gln	Lys	Pro	
Gly 45	Gln	Ala	Pro	Arg	Leu 50	Leu	Ile	Tyr	Ala	Ala 55	Ser	Asn	Leu	Glu	Ser 60	
Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro

105

100





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Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
                                         135
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                                     150
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
            160
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
                            180
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
    190
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205
                    210
                                         215
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      antibody
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                                           Met Glu Thr Asp Thr
                                            -20
atc ctg cta tgg gtg ctg ctc tgg gtt cca ggc tcc act ggt gag
                                                                   102
Ile Leu Leu Trp Val Leu Leu Trp Val Pro Gly Ser Thr Gly Glu
-15
                                                          - 1
att gtg ctc acc caa tct cca ggt act ttg tct ctg tct cca ggg gag
                                                                   150
Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
                                 10
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agg gcc ac Arg Ala Th 2	r Leu Ser	tgc aag Cys Lys	gcc Ala 25	agc Ser	caa Gln	agt Ser	gtt Val	gat Asp 30	tat Tyr	gat Asp	ggt Gly	198
gat agt ta Asp Ser Ty 35	t atg aac r Met Asn	tgg tac Trp Tyr 40	Gln	cag Gln	aaa Lys	cca Pro	gga Gly 45	cag Gln	gca Ala	ccc Pro	aga Arg	246
ctc ctc at Leu Leu Il 50	c tat gct e Tyr Ala	gca tcc Ala Ser 55	aat Asn	ctc Leu	gaa Glu	tct Ser 60	gly ggg	atc Ile	cca Pro	gac Asp	agg Arg 65	294
ttt agt gg Phe Ser Gl												342
gtg <u>g</u> ag ga Val Glu Gl	g gag gat u Glu Asp 85	gct gca Ala Ala	acc Thr	tat Tyr 90	tac Tyr	tgt Cys	cag Gln	caa Gln	agt Ser 95	aat Asn	gag Glu	390
gat cct cg Asp Pro Ar 10	g Thr Phe	ggt caa Gly Gln	ggc Gly 105	acc Thr	aag Lys	ctg Leu	gaa Glu	atc Ile 110	aaa Lys	cgg Arg	act Thr	438
gtg gct gc Val Ala Al 115	a cca tct a Pro Ser	gtc ttc Val Phe 120	atc Ile	ttc Phe	ccg Pro	cca Pro	tct Ser 125	gat Asp	gag Glu	cag Gln	ttg Leu	486
aaa tct gg Lys Ser Gl 130	a act gcc y Thr Ala	tct gtt Ser Val 135	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	534
aga gag gc Arg Glu Al	c aaa gta a Lys Val 150	cag tgg Gln Trp	aaa Lys	gtg Val	gat Asp 155	aac Asn	gcc Ala	ctc Leu	caa Gln	tcg Ser 160	Gly	582
aac tcc ca Asn Ser Gl												630
agc ctc ag Ser Leu Se 18	r Ser Thr											678
aaa gtc ta Lys Val Ty 195												726
aca aag ag Thr Lys Se 210					tagt	aaga	aat t	cggg	Ŧ			768

<210> 109





<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 109

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
-20 -15 -10 -5

Gly Ser Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
-1 1 5 10

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 30 35 40

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 45 50 55 60

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
65 70 75

Leu Thr Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 80 85 90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu 95 100 105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 125 130 135 140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 145 150 155

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 160 165 170

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
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Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 190 195 200

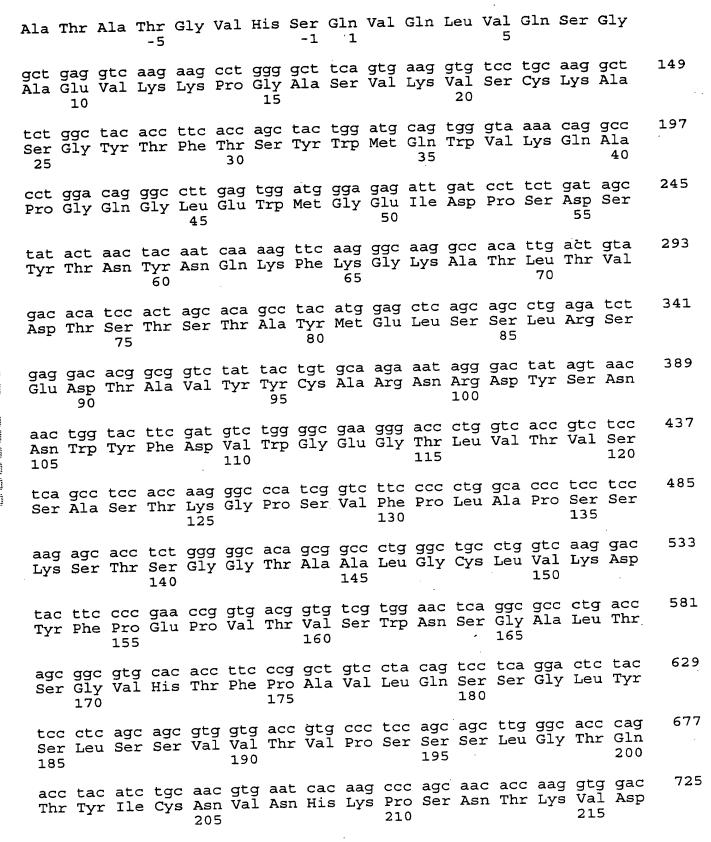
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215

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<210><211><212><212><213>	29	·•
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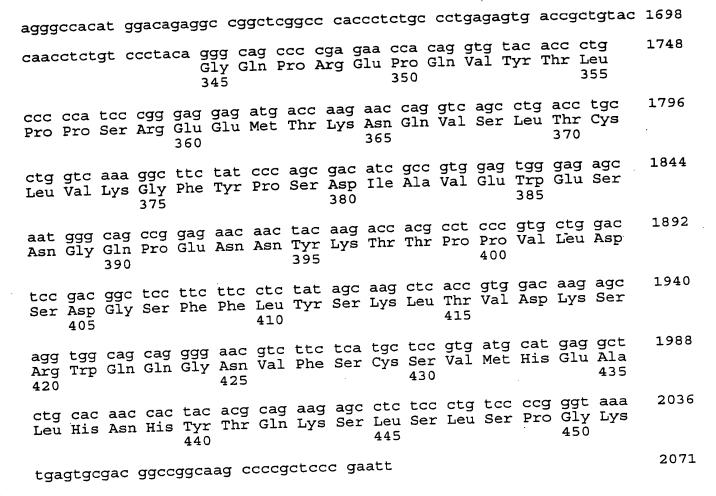
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                                                                    31
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<212> DNA
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      chain of a humanized anti-Fas antibody
                                                                    31
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يوم موجود مايو و حمول مايو

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                                                              -10
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                                                                      101
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aag aga gtt ggtgagaggc cagcacaggg agggagggcg cocgooggan Lys Arg Val	774
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aaggcaggcc ccgtctgcct cttcacccgg aggcctctgc ccgccccact catgctcagg	894
gagagggtct tctggctttt tccccaggct ctgggcaggc acaggctagg tgcccctaac	954
ccaggccctg cacacaaagg ggcaggtgct gggctcagac ctgccaagag ccatatccgg	1014
gaggaccetg ceeetgacet aageeeacee caaaggeeaa actetecaet eeeteagete	1074
ggacacette teteeteeca gatteeagta acteecaate ttetetetge a gag eee Glu Pro 220	1131
aaa tot tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro 225 230	1180
cccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg	1240
gacaggcccc agcegggtgc tgacacgtcc acctccatct cttcctca gca cct gaa Ala Pro Glu 235	1297
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 240 245 250	1345
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 255 260 265	1393
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 270 275 280 285	1441
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 290 295 300	1489
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp 305 310 315	1537
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro 320 325 330	1585
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<210> 117

<211> 470

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe



Thr 30	Ser	Tyr	Trp	Met	Gln 35	Trp	Val	Lys	Gln	Ala 40	Pro	Gly	Gln	Gly	Leu 45
Glu	Trp	Met	Gly	Glu 50	Ile	Asp	Pro	Ser	Asp 55	Ser	Tyr	Thr	Asn	Tyr 60	Asn
Gln	Lys	Phe	Lys 65	Gly	Lys	Ala	Thr	Leu 70	Thr	Val	Asp	Thr	Ser 75	Thr	Ser
Thr	Ala	Tyr 80	Met	Glu	Leu	Ser	Ser 85	Leu	Arg	Ser	Glu	Asp 90	Thr	Ala	Val
Tyr	Tyr 95	Cys	Ala	Arg	Asn	Arg 100	Asp	Tyr	Ser	Asn	Asn 105	Trp	Tyr	Phe	Asp
Val 110	Trp	Gly	Glu	Gly	Thr 115	Leu	Val	Thr	Val	Ser 120	Ser	Ala	Ser	Thr	Lys 125
Gly	Pro	Ser	Val	Phe 130	Pro	Leu	Ala	Pro	Ser 135	Ser	Lys	Ser	Thr	Ser 140	Gly
Gly	Thr	Ala	Ala 145	Leu	Gly	Cys	Leu	Val 150	Ļys	Asp	Tyr	Phe	Pro 155	Glu	Pro
Val	Thr	Val 160	Ser	Trp	Asn	Ser	Gly 165	Ala	Leu	Thr	Ser	Gly 170	Val	His	Thr
Phe	Pro 175	Ala	Val	Leu	Gln	Ser 180	Ser	Gly	Leu	Tyr	Ser 185	Leu	Ser	Ser	Val
Val 190	Thr	Val	Pro	Ser	Ser 195	Ser	Leu	Gly	Thr	Gln 200	Thr	Tyr	Ile	Cys	Asn 205
Val	Asn	His	Lys	Pro 210	Ser	Asn	Thr	Lys	Val 215	Asp	Lys	Arg	Val	Glu 220	Pro
Lys	Ser	Cys	Asp 225	Lys	Thr	His	Thr	Cys 230	Pro	Pro	Cys	Pro	Ala 235	Pro	Glu
Leu	Leu	Gly 240		Pro	Ser	Val	Phe 245	Leu	Phe	Pro	Pro	Lys 250	Pro	Lys	Asp
Thr	Leu 255		Ile	Ser	Arg	Thr 260	Pro	Glu	Val	Thr	Cys 265	Val	Val	Val	Asp
Val 270		His	Glu	Asp	Pro 275		Val	Lys	Phe	Asn 280	Trp	Tyr	Val	Asp	Gly 285
Val	Glu	. Val	. His	Asn 290		Lys	Thr	. Lys	Pro 295	Arg	Glu	Glu	Gln	Tyr 300	Asn
Ser	Thr	Tyr	Arg 305		. Val	Ser	· Val	Leu 310	Thr	· Val	. Leu	His	Gln 315	Asp	Trp

<220>





		320					323	Lys				J J0				
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Pro 350	Gln	Val	Tyr	Thr	Leu 355	Pro	Pro	Ser	Arg	Glu 360	Glu	Met	Thr	Lys	Asn 365	
Gln	Val	Ser	Leu	Thr 370	Cys	Leu	Val	Lys	Gly 375	Phe	Tyr	Pro	Ser	Asp 380	Ile	
Ala	Val	Glu	Trp 385	Glu	Ser	Asn	Gly	Gln 390	Pro	Glu	Asn	Asn	Tyr 395	Lys	Thr	
Thr	Pro	Pro 400		Leu	Asp	Ser	Asp 405	Gly	Ser	Phe	Phe	Leu 410	Tyr	Ser	Lys	
Leu	Thr 415		Asp	Lys	Ser	Arg 420	Trp	Gln	Gln	Gly	Asn 425	Val	Phe	Ser	Cys	
Ser 430		Met	His	Glu	Ala 435	Leu	His	Asn	. His	Tyr 440	Thr	Gln	Lys	Ser	Leu 445	
Ser	Leu	Ser	Pro	Gly 450	Lys	1										
<21 <21	L0> 1 L1> 3 L2> I L3> I	0 ONA	Eicia	al Se	equer	ıce										
<22 <22		amm]	i faz :	a fr:	acmei	nt o	ca 1	l Sec DNA e i-Fa:	211000	21119	CITE	orime heav	er to 7y	o		
<4 ca	ggcc	118 cctg	gac	aggg	cct '	tgag	tgga	tg								30
<2 <2	10> 11> 12> 13>	30 DNA	fici	al S	eque	nce					•					

<400> 119 catccactca aggccctgtc caggggcctg

30

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of a DNA encoding the heavy chain of a humanized anti-Fas antibody

<210> 120 <211> 39 <212> DNA <213> Artificial Sequence	s.
<220> <223> Description of Artificial Sequence: PCR primer to <223> Description of a DNA encoding the heavy amplify a fragment of a DNA entity and the heavy chain of a humanized anti-Fas antibody	
<400> 120 gctgagctcc atgtaggctg tgctagtgga tgtgtctac	39
<210> 121 <211> 33 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: PCR primer to amplify a DNA fragment including SR alpha promoter <400> 121 tgcacgcgtg gctgtggaat gtgtgtcagt tag	33
<210> 122 <211> 31 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer to <223> Description of Artificial Sequence: PCR primer to amplify a DNA fragment including SR alpha promoter <400> 122 tccgaagctt ttagagcaga agtaacactt c	31
<210> 123 <211> 36 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer to <223> Description of Artificial Sequence: PCR primer to amplify a DNA fragment including SR alpha promoter <400> 123 aaagcggccg ctgctagctt ggctgtggaa tgtgtg	36

<210> 124 <211> 34 <212> DNA <213> Artificial Sequence <220>

<223> Description of Artificial Sequence: PCR primer to amplify a DNA encoding the kappa light chain of human immunoglobulin

<400> 124
aagcttatgg acatgagggt ccccgctctg ctcc

34

<210> 125 <211> 729 <212> DNA <213> Homo sapiens

4400> 125
aagettatggacatgagggtcccegetetgctcetagggctcctgtaggctggetecgggtgccagatgtgacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacagagtcaccatcacttgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatcaaggttcagtggcagtggatctgggacagatttcactctcaccatcagcaggttcgaacctgaagattttgcaacttactactgtcaacagagttacagtacccetcgaacgttcggcaagggaccaaggtggaaatcaaacgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatctggaactgcctctgttgtgtgctgctgctataaacttctatcccaagagggccaaagtacagtggaaggtggataacgccctccaatcgggtaaccctgacgctgagcaaagcagcacaagacagcacctacagcctcaagagcaccctgacgctgagcaaagcagaaccaaagagcaccaacaggggagactgctaagtcacccatcagggcctgagctcgccgtcaccaagagcttcaacaggggagagtgttagtaa720gaattcgggtctgaatcggggcctgaaccaaagagcttcaacaggggagagtgttagtaa729

<210> 126 <211> 767 <212> DNA <213> Artificial Sequence

<220> <223> Description of Artificial Sequence: Designed DNA encoding the light chain of a humanized anti-Fas antibody
<220> <221> CDS <222> (39)(752)
<220> <221> mat peptide <222> (99)(752)
<220> <221> sig peptide <222> (39)(98)
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ctg cta tgg gtg ctg ctc tgg gtt cca ggc tcc act ggt gac att 104 Leu Leu Trp Val Leu Leu Trp Val Pro Gly Ser Thr Gly Asp Ile -10 -5 -1 1
gtg ctc acc caa tct cca tcc tcc ctg tct gca tct gta gga gac aga 152 Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 5
gtc acc atc act tgc aag gcc agc caa agt gtt gat tat gat ggt gat 200 Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp 20 25 30
agt tat atg aac tgg tac caa cag aaa cca gga aag gca ccc aag ctc 248 Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu 35 40 45 50
ctc atc tat gct gca tcc aat ttg gaa agt ggg gtc cca tca agg ttc 296 Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser Arg Phe 55 60 65
agt gga agt gga tct ggg aca gat ttt act ctc acc atc agc agc ctg 344 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu 70 75 80
cag cct gaa gat ttt gca acc tac tac tgt cag caa agt aac gag gat 392 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp 85 90 95
cct cgg acg ttc ggc caa ggc acc aag gtg gaa atc aaa cgg act gtg 440 Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val 100 105 110

gct g Ala A 115	rca la:	cca Pro	tct Ser	gtc Val	ttc Phe 120	atc Ile	ttc Phe	ccg Pro	cca Pro	tct Ser 125	gat Asp	gag Glu	cag Gln	ttg Leu	aaa Lys 130	488
tct g Ser G	ga Hy	act Thr	gcc Ala	tct Ser 135	gtt Val	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	aga Arg	536
gag g Glu A	gcc Ala	aaa Lys	gta Val 150	cag Gln	tgg Trp	aaa Lys	gtg Val	gat Asp 155	Asn	gcc Ala	ctc Leu	caa Gln	tcg Ser 160	ggt Gly	aac Asn	584
tcc c Ser G	ln	gag Glu 165	agt Ser	gtc Val	aca Thr	gag Glu	cag Gln 170	gac Asp	agc Ser	aag Lys	gac Asp	agc Ser 175	acc Thr	tac Tyr	agc Ser	632
ctc a Leu S 1	agc Ser L80	agc Ser	acc Thr	ctg Leu	acg Thr	ctg Leu 185	agc Ser	aaa Lys	gca Ala	gac Asp	tac Tyr 190	gag Glu	aaa Lys	cac His	aaa Lys	680
gtc t Val T 195	ac Tyr	gcc Ala	tgc Cys	gaa Glu	gtc Val 200	acc Thr	cat His	cag Gln	ggc Gly	ctg Leu 205	agc Ser	tcg Ser	ccc Pro	gtc Val	aca Thr 210	728
aag a Lys S	agc Ser	ttc Phe	aac Asn	agg Arg 215	gga Gly	gag Glu	tgt Cys	tagi	caaga	aat 1	tcgg	3				767

<210> 127

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 127

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
-20 -15 -10 -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser -1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 30 40

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 45 50 55 60







Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 115 110 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 140 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 170 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 215 210 205 <210> 128. <211> 767 <212> DNA <213> Artificial Sequence <220>

<223> Description of Artificial Sequence: Designed DNA encoding the light chain of a humanized anti-Fas antibody

<220>

<221> CDS

<222> (39)..(752)

<220>

<221> mat peptide

<222> (99)..(752)

<220>

<221> sig peptide

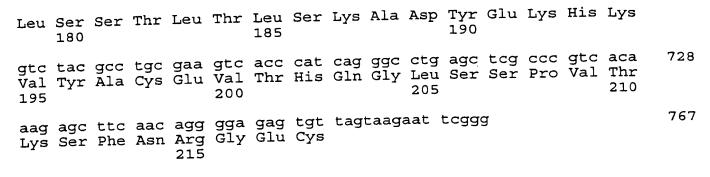
<222> (39)..(98)

<400> 128





ccaa	gctt.	aa g	aago	atcc	t ct	catc	tagt	tct	caga	ng at Me -2	t Gl	g ac u Th	a ga r As	c ac p Th	a atc r Ile -15	56
ctg Leu	cta Leu	tgg Trp	gtg Val	ctg Leu -10	ctg Leu	ctc Leu	tgg Trp	gtt Val	cca Pro -5	ggc Gly	tcc Ser	act Thr	ggt Gly -1	gac Asp 1	att Ile	104
gtg Val	ctc Leu	acc Thr 5	caa Gln	tct Ser	cca Pro	tcc Ser	tcc Ser 10	ctg Leu	tct Ser	gca Ala	tct Ser	gta Val 15	gga Gly	gac Asp	aga Arg	152
gtc Val	acc Thr 20	atc Ile	act Thr	tgc Cys	aag Lys	gcc Ala 25	agc Ser	caa Gln	agt Ser	gtt Val	gat Asp 30	tat Tyr	gat Asp	ggt Gly	gat Asp	200
agt Ser 35	tat Tyr	atg Met	aac Asn	tgg Trp	tac Tyr 40	caa Gln	cag Gln	aaa Lys	cca Pro	gga Gly 45	cag Gln	gca Ala	ccc Pro	aag Lys	ctc Leu 50	248
ctc Leu	atc Ile	tat Tyr	gct Ala	gca Ala 55	tcc Ser	aat Asn	ttg Leu	gaa Glu	agt Ser 60	Gly ggg	gtc Val	cca Pro	tca Ser	agg Arg 65	ttc Phe	296
agt Ser	gga Gly	agt Ser	gga Gly 70	tct Ser	gly ggg	aca Thr	gat Asp	ttt Phe 75	act Thr	ctc Leu	acc Thr	atc Ile	agc Ser 80	agc Ser	ctg Leu	344
cag Gln	cct Pro	gaa Glu 85	gat Asp	ttt Phe	gca Ala	acc Thr	tac Tyr 90	tac Tyr	tgt Cys	caa Gln	cag Gln	agt Ser 95	aac Asn	gag Glu	gat Asp	392
cct Pro	cga Arg 100	acg Thr	ttc Phe	ggc Gly	caa Gln	ggc Gly 105	acc Thr	aag Lys	gtg Val	gaa Glu	atc Ile 110	aaa Lys	cgg Arg	act Thr	gtg Val	440
gct Ala 115	gca Ala	cca Pro	tct Ser	gtc Val	ttc Phe 120	atc Ile	ttc Phe	ccg Pro	cca Pro	tct Ser 125	gat Asp	gag Glu	cag Gln	ttg Leu	aaa Lys 130	488
tct Ser	gga Gly	act Thr	gcc Ala	tct Ser 135	gtt Val	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	aga Arg	536
gag Glu	gcc Ala	aaa Lys	gta Val 150	cag Gln	tgg Trp	aaa Lys	gtg Val	gat Asp 155	aac Asn	gcc Ala	ctc Leu	caa Gln	tcg Ser 160	ggt Gly	aac Asn	584
tcc Ser	cag Gln	gag Glu 165	Ser	gtc Val	aca Thr	gag Glu	cag Gln 170	gac Asp	agc Ser	aag Lys	gac Asp	agc Ser 175	acc Thr	tac Tyr	agc Ser	632
ctc	ago	ago	acc	ctg	acg	ctg	agc	aaa	gca	. gac	tac	gag	aaa	cac	aaa	680



<210> 129 <211> 238 <212> PRT <213> Artificial Sequence

<400> 129
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro
-10 -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 30 35 40

Gly Gln Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 45 50 55 60

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr 65 70 75

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
-80 85 90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 110 115 : 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 125 130 135 140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 145

Ala	Leu	Gln	Ser 160	Gly	Asn	Ser	Gln	Glu 165	Ser	Val	Thr	Glu	Gln 170	Asp	Ser	
Lys	Asp	Ser 175	Thr	Tyr	Ser	Leu	Ser 180	Ser	Thr	Leu	Thr	Leu 185	Ser	Lys	Ala	
Asp	Tyr 190	Glu	Lys	His	Lys	Val 195	Tyr	Ala	Cys	Glu	Val 200	Thr	His	Gln	Gly	
Leu 205	Ser	Ser	Pro	Val	Thr 210	Lys	Ser	Phe	Asn	Arg 215	Gly	Glu	Cys			
<21 <21	0 > 1 1 > 7 2 > D 3 > A	78 NA	icia	l Se	quen	ce										
<22 <22	3> D e	escr ncod ntib	ing	on o the	f Ar ligh	tifi t ch	cial ain	Seq of a	uenc hum	e: D aniz	esig ed a	ned I nti-I	ONA Fas			
	0> 1> C 2> (. (75	52)												
	10> 11> π 22> (
	20> 21> s 22>															
<4(00> 3 aagct	130 ctaa	gaag	gcato	ect (ctcat	ctag	gt to	ctcag	1,	atg g Met G	gag a Slu T	ca c	ac a Asp l	aca ato Thr Ile	-
ct; Le:	g cta u Le	a tgg u Trj	g gt p Va	g ctg l Le -1	u Lei	g cto u Le	c tgg u Trj	g gt p Va	t cca l Pro) GT	c tco y Sei	act Thr	ggt Gly	AS	c att p Ile i	104
gt: Va	g ct l Le	u Th	c ca r Gl 5	a tc n Se	t cc r Pr	a tc o Se	c tc r Se . 1	rье	g tc u Se:	t gca r Ala	a tci a Sei	t gta r Val	- GT	a gad Y Asj	c aga o Arg	152
gt Va	c ac 1 Th 2	r Il	c ac e Th	t tg r Cy	c aa s Ly	g gc s Al 2	a Se	c ca r Gl	a ag n Se	t gt r Va	t ga l As _l 3	Б тАл	ga Asj	t gg	t gat y Asp	200
ag	t ta	t at	g aa	ıc tg	g ta	.с са	a ca	g aa	a cc	a gg	a aa	g gca	a cc	c aa	a ctc	248



Ser 35	Tyr	Met	Asn	Trp	Tyr 40	Gln	Gln	Lys	Pro	Gly 45	Lys	Ala	Pro	Lys	Leu 50	
ctc Leu	atc Ile	tac Tyr	gct Ala	gca Ala 55	tcc Ser	aat Asn	ttg Leu	gaa Glu	tca Ser 60	gly ggg	atc Ile	cca Pro	tca Ser	agg Arg 65	ttc Phe	296
agt Ser	gga Gly	agt Ser	gga Gly 70	tct Ser	gly aaa	aca Thr	gat Asp	ttt Phe 75	act Thr	ctc Leu	acc Thr	atc Ile	agc Ser 80	agc Ser	ctg Leu	344
cag Gln	cct Pro	gag Glu 85	gat Asp	ttt Phe	gca Ala	acc Thr	tat Tyr 90	tac Tyr	tgt Cys	cag Gln	caa Gln	agt Ser 95	aat Asn	gag Glu	gat Asp	392
cct Pro	cgg Arg 100	acg Thr	ttc Phe	ggt Gly	caa Gln	ggc Gly 105	acc Thr	aag Lys	gtg Val	gaa Glu	atc Ile 110	aaa Lys	cgg Arg	act Thr	gtg Val	440
gct Ala 115	gca Ala	cca Pro	tct Ser	gtc Val	ttc Phe 120	atc Ile	ttc Phe	ccg Pro	cca Pro	tct Ser 125	gat Asp	gag Glu	cag Gln	ttg Leu	aaa Lys 130	488
tct Ser	gga Gly	act Thr	gcc Ala	tct Ser 135	gtt Val	gtg Val	tgc Cys	ctg Leu	ctg Leu 140	aat Asn	aac Asn	ttc Phe	tat Tyr	ccc Pro 145	aga Arg	536
gag Glu	gcc Ala	aaa Lys	gta Val 150	cag Gln	tgg Trp	aag Lys	gtg Val	gat Asp 155	aac Asn	gcc Ala	ctc Leu	caa Gln	tcg Ser 160	ggt Gly	aac Asn	584
tcc Ser	cag Gln	gag Glu 165	Ser	gtc Val	aca Thr	gag Glu	cag Gln 170	gac Asp	agc Ser	aag Lys	gac Asp	agc Ser 175	acc Thr	tac Tyr	agc Ser	632
ctc Leu	agc Ser 180	Ser	acc Thr	ctg Leu	acg Thr	ctg Leu 185	Ser	aaa Lys	gca Ala	gac Asp	tac Tyr 190	gag Glu	aaa Lys	cac His	aaa Lys	680
gtc Val 195	Tyr	gcc Ala	tgc Cys	gaa Glu	gtc Val 200	Thr	cat His	cag Gln	ggc Gly	ctg Leu 205	ser	tcg Ser	ccc Pro	gtc Val	aca Thr 210	728
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<220>

<210> 131 <211> 238 <212> PRT <213> Artificial Sequence

<223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 131
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-20 -15 -10 -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro 30 35 40

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser 45 50 55 60

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 65 70 75

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys 80 85 90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val 95 100 105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu 125 130 135 140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 145 150 155

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser 160 165 170

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala 175 180 185

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly 190 195 200

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215

<210> 132

<211> 41

<212> DNA

	<213> Artificial Sequence	
	<220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody	
	<400> 132 agggaggatg gagattgggt gagcacaatg tcaccagtgg a	41
	<210> 133 <211> 39 <212> DNA <213> Artificial Sequence	
The state of the s	<pre><220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody</pre>	
	<400> 133 attgtgctca cccaatctcc atcctccctg tctgcatct	39
May 15 and 16 an	<210> 134 <211> 42 <212> DNA <213> Artificial Sequence	
	<220>	
, Figerra	<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody	
	<400> 134 atcaacactt tggctggcct tgcaagtgat ggtgactctg tc	42
	<210> 135 <211> 40 <212> DNA <213> Artificial Sequence	
	<pre><220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody</pre>	
	<400> 135 ccatcacttg caaggccagc caaagtgttg attatgatgg	40

	<210> 136 <211> 48 <212> DNA <213> Artificial Sequence	
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	<400> 136 agtttcgaga ttggatgcag catagatgag gagtttgggt gcctttcc	48
Print II.	<210> 137 <211> 45 <212> DNA <213> Artificial Sequence	
And the first that the first that	<pre><220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody</pre>	
.	<400> 137 cccaagetee teatetatge tgeatecaat ttggaaagtg gggte	45
	<211> 44 <212> DNA	
	<220>	
	<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody	
	<400> 138 ttggccgaac gttcgaggat cctcgttact ctgttgacag tagt	44
	<210> 139 <211> 44 <212> DNA <213> Artificial Sequence	
	<pre><220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody</pre>	
	<400> 139	

	actact	gtca acagagtaac gaggateete gaaegttegg eeaa	44
	<210><211><211><212><213>	45	
	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody	
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The first first of the first first	<210><211><212><212><213>	45	
	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody	
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	<210><211><211><212><213>	2073	
	<220>		
	<223>	Description of Artificial Sequence: Designed DNA encoding the heavy chain of a humanized anti-Fas antibody	
		sig peptide (23)(79)	
		intron (737)(1127)	
		. intron (1290)	

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<220>
   <221> intron
   <222> (1621)..(1717)
   <220>
   <221> exon
   <222> (23)..(736)
   <220>
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   <220>
   <221> exon
#I
   <222> (1718)..(2038)
11
   <220>
   <221> mat peptide
   <222> (80)..(736)
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Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr 185 190 195	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val 200 215	724
gac aag aga gtt ggtgagaggc cagcacaggg agggagggtg tctgctggaa Asp Lys Arg Val	776
gccaggctca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc	836
aaggcaggcc ccgtctgcct cttcacccgg aggcctctgc ccgccccact catgctcagg	896
gagagggtct tetggetttt teeceagget etgggeagge acaggetagg tgeecetaae	956
ccaggccctg cacacaaagg ggcaggtgct gggctcagac ctgccaagag ccatatccgg	1016
gaggaccetg eccetgacet aageceaeee caaaggeeaa actetecaet eccteagete	1076
ggacacette tetectecca gattecagta acteccaate ttetetetge a gag eec Glu Pro 220	1133
aaa tot tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro 225 230	1182
cccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg	1242
gacaggeece ageegggtge tgacaegtee acetecatet etteetea gea eet gaa Ala Pro Glu 235	1299
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 240 245 250	1347
Leu Leu Gly Gly Pro Ser var File Bed 1116 250	1347 1395
Leu Leu Gly Gly Pro Ser Val Phe Bott The 250 acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr 260 gtg agc cac gaa gac cct gag gtc aag ttc aac tgc ytg gtg gtg gac 265 gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 285	1395 1443
Leu Leu Gly Gly Pro Ser Val Phe Hea The Leu File Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 265 gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 285	1395

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro 320 325 330	1587
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys 335 340	1640
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caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu 345 350 355	1750
ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys 360 365 370	1798
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aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp 390 395 400	1894
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ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 440 445 450	2038
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<210> 143

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<400> 143

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser 70 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys 125 120 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 135 130 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 150 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 165 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 200 195 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro 210 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu 230 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 245 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 265 260 255 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 280 275 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 300 295 290 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp 310 305 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro 330 325 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 340 335 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 355 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 390 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 405 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 415 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 440 435 430

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<210> 144
<211> 2073
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<212> DNA

<213> Artificial Sequence

Ser Leu Ser Pro Gly Lys

<220>

<223> Description of Artificial Sequence: Designed DNA encoding the heavy chain of a humanized anti-Fas antibody

<220>

<221> sig peptide

<222> (23)..(79)

<220>

<221> intron

<222> (737)..(1127)

<220>

- <221> intron

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   <222> (1621)..(1717)
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Gly aaa	gct Ala	gag Glu 10	gtc Val	aag Lys	aag Lys	cct Pro	ggg Gly 15	gct Ala	tca Ser	gtg Val	aag Lys	gtg Val 20	tcc Ser	tgc Cys	aag Lys	148
gct Ala	tct Ser 25	ggc Gly	tac Tyr	acc Thr	ttc Phe	acc Thr 30	agc Ser	tac Tyr	tgg Trp	atg Met	cag Gln 35	tgg Trp	gta Val	aaa Lys	cag Gln	196
		gga Gly														244
		act Thr														292
		aca Thr														340
tct Ser	gag Glu	gac Asp 90	acg Thr	gcg Ala	gtc Val	tat Tyr	tac Tyr 95	tgt Cys	gca Ala	aga Arg	aat Asn	agg Arg 100	gac Asp	tat Tyr	agt Ser	388
		tgg Trp														436
		gcc Ala														484
		agc Ser														532
		ttc Phe														580
		ggc Gly 170														628
tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	676

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr 185 190 195	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val 200 215	724
gac aag aga gtt ggtgagaggc cagcacaggg agggagggtg tctgctggaa Asp Lys Arg Val	776
gccaggctca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc	836
aaggcaggcc ccgtctgcct cttcacccgg aggcctctgc ccgccccact catgctcagg	
gagagggtet tetggetttt teeceagget etgggeagge acaggetagg tgeecetaae	
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gaggaccetg cecetgacet aageecacee caaaggecaa aetetecaet eeeteagete	
ggacacette teteeteeca gatteeagta acteecaate ttetetetge a gag eee Glu Pro 220	1133
aaa tot tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro 225 230	1182
cccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg	1242
gaçaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa Ala Pro Glu 235	1299
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 240 245 250	1347
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 255 260 265	1395
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 270 285	1443
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 290 295 300	1491
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	1539



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g A	cc la	ccc Pro 335	atc Ile	gag Glu	aaa Lys	acc Thr	atc Ile 340	tcc Ser	aaa Lys	gcc Ala	aaa Lys	ggtg	ggac	cc g	ıtggg	gtgcg	1640
a	ggg	cca	cat c	gaca	agagg	ic cō	gcto	ggc	cad	ccctc	tgc	ccto	gagag	rtg a	accgo	tgtac	1700
C	aac	ctct	gt (ccta		ggg (31y (345	ag o	ecc o Pro <i>l</i>	ga g Arg (Glu E	ca (ro (150	eag g Sln V	gtg t Val T	ac a Yr 1	acc c Thr I	etg Leu 155	1750
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	ctg Leu	gtc Val	aaa Lys	ggc Gly 375	ttc Phe	tat Tyr	ccc Pro	agc Ser	gac Asp 380	atc Ile	gcc Ala	gtg Val	gag Glu	tgg Trp 385	gag Glu	agc Ser	1846
i F	aat Asn	gly ggg	cag Gln 390	ccg Pro	gag Glu	aac Asn	aac Asn	tac Tyr 395	aag Lys	acc Thr	acg Thr	cct Pro	ccc Pro 400	gtg Val	ctg Leu	gac Asp	1894
ing ind and that that the first	ccc Ser	gac Asp 405	Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu 410	tat Tyr	agc Ser	aag Lys	ctc Leu	acc Thr 415	gtg Val	gac Asp	aag Lys	agc Ser	1942
-	agg Arg 420	tgg Trp	cag Gln	cag Gln	Gly	aac Asn 425	gtc Val	ttc Phe	tca Ser	tgc Cys	tcc Ser 430	gtg Val	atg Met	cat His	gag Glu	gct Ala 435	1990
]	ctg Leu	cac His	aac Asn	cac His	tac Tyr 440	acg Thr	cag Gln	aag Lys	agc Ser	ctc Leu 445	tcc Ser	ctg Leu	tcc Ser	ccg Pro	ggt Gly 450	aaa Lys	2038
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<210> 145

<211> 470

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Designed heavy chain of humanized anti-Fas antibody

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Val	His	Ser -1	Gln 1	Val	Gln	Leu	Val 5	Gln	Ser	Gly	Ala	Glu 10	Val	Lys	Lys
Pro	Gly 15	Ala	Ser	Val	Lys	Val 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Tyr	Thr	Phe
Thr 30	Ser	Tyr	Trp	Met	Gln 35	Trp	Val	Lys	Gln	Ala 40	Pro	Gly	Gln	Gly	Leu 45
Glu	Trp	Met	Gly	Glu 50	Ile	Asp	Pro	Ser	Asp 55	Ser	Tyr	Thr	Asn	Tyr 60	Asn
Gln	Lys	Phe	Lys 65	Gly	Lys	Ala	Thr	Ile 70	Thr	Val	Asp	Thr	Ser 75	Thr	Ser
Thr	Ala	Tyr 80	Met	Glu	Leu	Ser	Ser 85	Leu	Arg	Ser	Glu	Asp 90	Thr	Ala	Val
Tyr	Tyr 95	Cys	Ala	Arg	Asn	Arg 100	Asp	Tyr	Ser	Asn	Asn 105	Trp	Tyr	Phe	Asp
Val 110	Trp	Gly	Gln	Gly	Thr 115	Leu	Val	Thr	Val	Ser 120	Ser	Ala	Ser	Thr	Lys 125
Gly	Pro	Ser	Val	Phe 130	Pro	Leu	Ala	Pro	Ser 135	Ser	Lys	Ser	Thr	Ser 140	Gly
Gly	Thr	Ala	Ala 145	Leu	Gly	Cys	Leu	Val 150	Lys	Asp	Tyr	Phe	Pro 155	Glu	Pro
Val	Thr	Val 160	Ser	Trp	Asn	Ser	Gly 165	Ala	Leu	Thr	Ser	Gly 170	Val	His	Thr
Phe	Pro 175	Ala	Val	Leu	Gln	Ser 180	Ser	Gly	Leu	Tyr	Ser 185	Leu	Ser	Ser	Val
Val 190	Thr	Val	Pro	Ser	Ser 195	Ser	Leu	Gly	Thr	Gln 200	Thr	Tyr	Ile	Cys	Asn 205
Val	Asn	His	Lys	Pro 210	Ser	Asn	Thr	Lys	Val 215	Asp	Lys	Arg	Val	Glu 220	Pro
Lys	Ser	Cys	Asp 225	Lys	Thr	His	Thr	Cys 230	Pro	Pro	Cys	Pro	Ala 235	Pro	Glu
Leu	Leu	Gly 240	Gly	Pro	Ser	Val	Phe 245	Leu	Phe	Pro	Pro	Lys 250	Pro	Lys	Asp
Thr	Leu 255	Met	Ile	Ser	Arg	Thr 260	Pro	Glu	Val	Thr	Cys 265	Val	Val	Val	Asp
Val 270	Ser	His	Glu	Asp	Pro 275	Glu	Val	Lys	Phe	Asn 280	Trp	Tyr	Val	Asp	Gly 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 300 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp 310 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 335 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 355 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 380 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 410 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 415 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 440 Ser Leu Ser Pro Gly Lys

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<210> 146
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<223> Description of Artificial Sequence: Designed DNA encoding the heavy chain of a humanized anti-Fas antibody

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<221> sig peptide

<222> (23)..(79)

<220>

<221> intron

<222> (737)..(1127)

<220>

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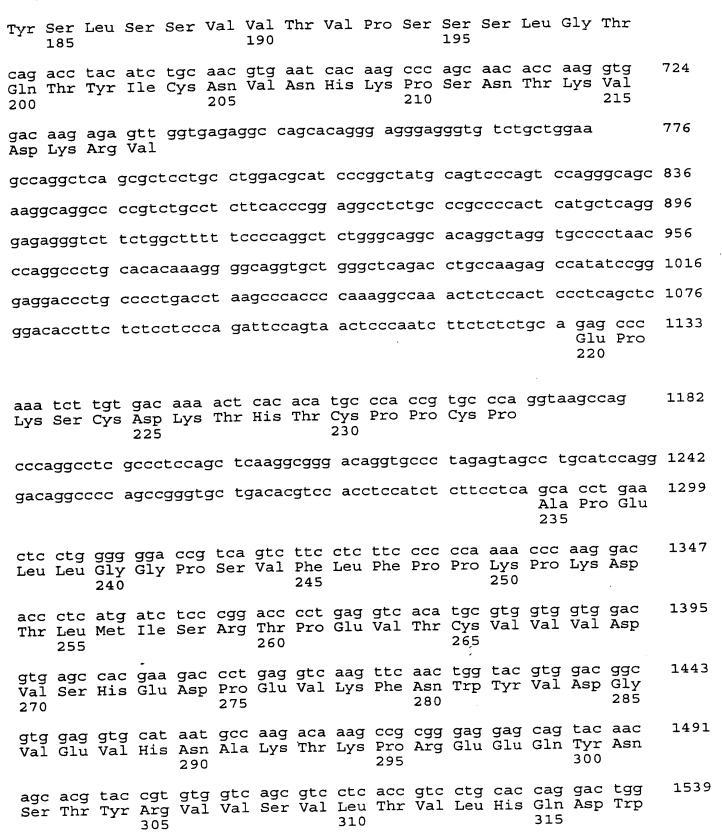
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<212> DNA

<213> Artificial Sequence

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ggg gct gag gtc aag aag cct ggg gct tca gtg aag gtg tcc tgc aag Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys 10 15 20	148
gct tct ggc tac acc ttc acc agc tac tgg atg cag tgg gta cga cag Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Arg Gln 25 30 35	196
gcc cct gga caa gga ctt gag tgg atg gga gag att gat cct tct gat 2 Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp 40 45 50	244
agc tat act aac tac aat caa aag ttc aag ggc aag gcc aca ttg act 2 Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr 60 65 70	292
gta gac aca tcc act agc aca gcc tac atg gag ctc agc agc ctg aga Val Asp Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg 75 80 85	340
tct gag gac acg gcg gtc tat tac tgt gca aga aat agg gac tat agt Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser 90 95 100	388
aac aac tgg tac ttc gat gtc tgg ggc caa ggt aca ctg gtc acc gtc Asn Asn Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val 105 110 115	436
tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser 120 125 130 135	484
tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys 140 145 150	532
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acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu 170 175 180	628
tac tee ete age age gtg gtg ace gtg eee tee age age ttg gge ace	676



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gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys 335 340	1640													
agggccacat ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac	1700													
caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu 345 350 355														
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ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser 375 380 385	1846													
aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp 390 395 400	1894													
tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser 405 410 415	1942													
agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala 420 425 430 435	1990													
ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 440 445 450	2038													
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<210> 147

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed heavy chain of humanized anti-Fas antibody

<400> 147 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly -10

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 85 Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp 105 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys 120 110 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 135 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 155 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 185 180 Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 205 190 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro 215 210 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu 235 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 250 240 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 265 260 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 285



Val	Glu	Val	His	Asn 290	Ala	Lys	Thr	Lys	Pro 295	Arg	Glu	Glu	Gln	Tyr 300	Asn
Ser	Thr	Tyr	Arg 305	Val	Val	Ser	Val	Leu 310	Thr	Val	Leu	His	Gln 315	Asp	Trp
Leu	Asn	Gly 320	Lys	Glu	Tyr	Lys	Cys 325	Lys	Val	Ser	Asn	Lys 330	Ala	Leu	Pro
Ala	Pro 335	Ile	Glu	Lys	Thr	Ile 340	Ser	Lys	Ala	Lys	Gly 345	Gln	Pro	Arg	Glu
Pro 350	Gln	Val	Tyr	Thr	Leu 355	Pro	Pro	Ser	Arg	Glu 360	Glu	Met	Thr	Lys	Asn 365
Gln	Val	Ser	Leu	Thr 370	Cys	Leu	Val	Lys	Gly 375	Phe	Tyr	Pro	Ser	Asp 380	Ile
Ala	Val	Glu	Trp 385	Glu	Ser	Asn	Gly	Gln 390	Pro	Glu	Asn	Asn	Tyr 395	Lys	Thr
Thr	Pro	Pro 400		Leu	Asp	Ser	Asp 405	Gly	Ser	Phe	Phe	Leu 410	Tyr	Ser	Lys
Leu	Thr 415		Asp	Lys	Ser	Arg 420	Trp	Gln	Gln	Gly	Asn 425	Val	Phe	Ser	Cys
Ser 430		Met	His	Glu	Ala 435	Leu	His	Asn	His	Tyr 440	Thr	Gln	Lys	Ser	Leu 445
Ser	Leu	Ser	Pro	Gly 450											

<210> 148

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody

<400> 148 ccaagcttgg cttgacctca ccatgggatg gagctgta

38

<210> 149

<211> 40

<212> DNA

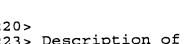
<213> Artificial Sequence

<220>

<	:223>	amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody	
ć	:400> agtggg	149 gtaaa acaggcccct ggacagggac ttgagtggat	40
٠	<210><211><212><212><213>	40	
•	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody	
	<400> atcca	150 ctcaa gtccctgtcc aggggcctgt tttacccact	40
	<210><211><212><212><213>	64	
	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody	
	<400> aagac	151 cgatg ggcccttggt ggaggctgag gagacggtga ccagtgtacc ttggccccag	
	acat		64
	<210 > <211 > <212 > <212 > <213 >	• 39	
	<220 × <223 ×	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody	
	<400: gttc:	: > 152 aagggc aaggccacaa taactgtaga cacatccgc	39
	<210	> 153	

<212> DNA <213> Artificial Sequence	
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<400> 153 gcggatgtgt ctacagttat tgtggccttg cccttgaac	39
<210> 154 <211> 40 <212> DNA <213> Artificial Sequence	
<pre><220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody</pre>	
<400> 154 agtgggtacg acaggcccct ggacaaggac ttgagtggat	40
<210> 155 <211> 40 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of a humanized anti-Fas antibody	
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<210> 156 <211> 2077 <212> DNA <213> Artificial Sequence	
<220> <221> sig peptide <222> (27)(83)	
<220> <221> intron <222> (741)(1131)	
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<221> intron <222> (1177)..(1294) <220> <221> intron <222> (1625)..(1725) <220> <221> exon <222> (27)..(740) <220> <221> exon <222> (1132)..(1176) <220> <221> exon <222> (1295)..(1624) <220> <221> exon <222> (1722)..(2042) <220> <221> mat peptide <222> (84)..(740) <220> <221> mat peptide <222> (1132)..(1176) <220> <221> mat peptide <222> (1295)..(1624) <220> <221> mat peptide <222> (1722)..(2042) <220> <221> CDS <222> (27)..(740) <220> <221> CDS <222> (1132)..(1176) <220> <221> CDS <222> (1295)..(1624) <220> <221> CDS <222> (1722)..(2042)





<220> <223> Description of Artificial Sequence: Designed DNA
 encoding the heavy chain of humanized anti-Fas
 antibody

<400 gggc	> 15 gaaa	igc t	tggc	ttga	ıc ct	cacc	ato Met	g gga : Gly	tgg Trp	ago Ser	tgt Cys -15	Ile	ato : Ile	cto Leu	ttc Phe	53
ttg Leu -10	gta Val	gca Ala	aca Thr	gct Ala	aca Thr -5	ggt Gly	gtc Val	cac His	tct Ser -1	cag Gln 1	gtc Val	caa Gln	ctg Leu	gtg Val 5	cag Gln	101
tct Ser	gly aaa	gct Ala	gag Glu 10	gtc Val	aag Lys	aag Lys	cct Pro	ggg Gly 15	gct Ala	tca Ser	gtg Val	aag Lys	gtg Val 20	tcc Ser	tgc Cys	149
aag Lys	gct Ala	tct Ser 25	ggc Gly	tac Tyr	acc Thr	ttc Phe	acc Thr 30	agc Ser	tac Tyr	tgg Trp	atg Met	cag Gln 35	tgg Trp	gta Val	cga Arg	197
cag Gln	gcc Ala 40	cct Pro	gga Gly	cag Gln	ggc Gly	ctt Leu 45	gag Glu	tgg Trp	atg Met	gga Gly	gag Glu 50	att Ile	gat Asp	cct Pro	tct Ser	245
gat Asp 55	agc Ser	tat Tyr	act Thr	aac Asn	tac Tyr 60	aat Asn	caa Gln	aag Lys	ttc Phe	aag Lys 65	ggc Gly	cgg Arg	gtc Val	aca Thr	atc Ile 70	293
act Thr	cga Arg	gac Asp	aca Thr	tcc Ser 75	act Thr	agc Ser	aca Thr	gcc Ala	tac Tyr 80	atg Met	gag Glu	ctc Leu	agc Ser	agc Ser 85	ctg Leu	341
aga Arg	tct Ser	gag Glu	gac Asp 90	acg Thr	gcg Ala	gtc Val	tat Tyr	tac Tyr 95	tgt Cys	gca Ala	aga Arg	aat Asn	agg Arg 100	gac Asp	tat Tyr	389
agt Ser	aac Asn	aac Asn 105	tgg Trp	tac Tyr	ttc Phe	gat Asp	gtc Val 110	tgg Trp	ggc Gly	gaa Glu	Gly	acc Thr 115	ctg Leu	gtc Val	acc Thr	437
gtc Val	tcc Ser 120	Ser	gčc Ala	tcc Ser	acc Thr	aag Lys 125	ggc Gly	cca Pro	tcg Ser	gtc Val	ttc Phe 130	ccc Pro	ctg Leu	gca Ala	ccc Pro	485
tcc Ser 135	Ser	aag Lys	agc Ser	acc Thr	tct Ser 140	Gly	ggc Gly	aca Thr	gcg Ala	gcc Ala 145	ctg Leu	ggc Gly	tgc Cys	ctg Leu	gtc Val 150	533
aag Lys	gac Asp	tac Tyr	ttc Phe	ccc Pro 155	Glu	ccg Pro	gtg Val	acg Thr	gtg Val 160	Ser	tgg Trp	aac Asn	tca Ser	ggc Gly 165	gcc Ala	581



ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly 170 175 180	629									
ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly 185 190 195	677									
acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys 200 205 210	725									
gtg gac aag aga gtt ggtgagaggc cagcacaggg agggagggtg tctgctggaa Val Asp Lys Arg Val 215	780									
gccaggctca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc	840									
aaggcaggcc ccgtctgcct cttcacccgg aggcctctgc ccgccccact catgctcagg	900									
gagagggtet tetggetttt teeccagget etgggeagge acaggetagg tgeecetaae	960									
ccaggccctg cacacaaagg ggcaggtgct gggctcagac ctgccaagag ccatatccgg	1020									
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aaa tot tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro 225 230	1186									
cccaggcctc gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg	1246									
gacaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa Ala Pro Glu 235										
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 240 . 245 . 250	1351									
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 255 260 265	1399									
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 270 275 280 285	1447									
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac	1495									





								_								
Val	Glu	Val	His	Asn 290	Ala	Lys	Thr	Lys	Pro 295	Arg	Glu	Glu	Gln	Tyr 300	Asn	
agc Ser	acg Thr	tac Tyr	cgt Arg 305	gtg Val	gtc Val	agc Ser	gtc Val	ctc Leu 310	acc Thr	gtc Val	ctg Leu	cac His	cag Gln 315	gac Asp	tgg Trp	1543
ctg Leu	aat Asn	ggc Gly 320	aag Lys	gag Glu	tac Tyr	aag Lys	tgc Cys 325	aag Lys	gtc Val	tcc Ser	aac Asn	aaa Lys 330	gcc Ala	ctc Leu	cca Pro	1591
gcc Ala	ccc Pro 335	atc Ile	gag Glu	aaa Lys	acc Thr	atc Ile 340	tcc Ser	aaa Lys	gcc Ala	aaa Lys	ggtg	ggac	ac g	gtggg	gtgcg	1644
aggg	gccad	cat q	ggaca	agagg	gc cs	gata	ggco	cad	cacto	ctgc	ccts	gagag	gtg a	accgo	ctgtac	1704
caad	cctct	gt (cccta	(ggg (Gly (345	cag o	ccc o Pro <i>l</i>	ega (Arg (Glu E	cca d Pro 0 350	cag g Sln V	gtg t /al 1	ac a Tyr T	Chr I	ctg Leu 355	1754
ccc Pro	cca Pro	tcc Ser	cgg Arg	gag Glu 360	gag Glu	atg Met	acc Thr	aag Lys	aac Asn 365	cag Gln	gtc Val	agc Ser	ctg Leu	acc Thr 370	tgc Cys	1802
ctg Leu	gtc Val	aaa Lys	ggc Gly 375	Phe	tat Tyr	ccc Pro	agc Ser	gac Asp 380	atc Ile	gcc Ala	gtg Val	gag Glu	tgg Trp 385	gag Glu	agc Ser	1850
aat Asn	Gly	cag Gln 390	Pro	gag Glu	aac Asn	aac Asn	tac Tyr 395	aag Lys	acc Thr	acg Thr	cct Pro	ccc Pro 400	gtg Val	ctg Leu	gac Asp	1898
tcc Ser	gac Asp 405	Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu 410	tat Tyr	agc Ser	aag Lys	ctc Leu	acc Thr 415	gtg Val	gac Asp	aag Lys	agc Ser	1946
agg Arg 420	Trp	cag Gln	cag Gln	ggg Gly	aac Asn 425	gtc Val	ttc Phe	tca Ser	tgc Cys	tcc Ser 430	gtg Val	atg Met	cat His	gag Glu	gct Ala 435	1994
ctg Leu	cac His	aac Asn	cac His	tac Tyr 440	Thr	cag Gln	aag Lys	agc Ser	ctc Leu 445	Ser	ctg Leu	tcc Ser	ccg Pro	ggt Gly 450	aaa Lys	2042
																0077

<210> 157

<211> 470

<212> PRT

<213> Artificial Sequence

tgagtgcgac ggccggcaag ccccgctccc gaatt

<220>







<223> Description of Artificial Sequence: Designed heavy chain of humanized anti-Fas antibody

<400> 157 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly -10 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser 75 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp 105 100 Val Trp Gly Glu Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys 120 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 135 130 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 150 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 165 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 180 185 Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 195 190 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro 215 210 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu 235 230 225 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 245 250





Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 260 265 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 280 275 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 290 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp 310 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro 330 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 340 335 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 365 355 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 370 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 390 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 405 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 420 415 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 440 430

Ser Leu Ser Pro Gly Lys 450

<210> 158

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of humanized anti-Fas antibody

<400> 158 gatgcagtgg gtacgacagg cccctggac

	<210><211><212><213>	29						
The second control of	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of humanized anti-Fas antibody						
	<400> gtccag	159 ggggc ctgtcgtacc cactgcatc	29					
	<210><211><211><212><213>	33						
	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of humanized anti-Fas antibody						
	<400> 160 caagggccgg gtcacaatca ctcgagacac atc 3:							
	<210><211><212><213>	33						
¹⁶ fee of	<220> <223>	Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the heavy chain of humanized anti-Fas antibody						
	<400> gatgt	161 gtctc gagtgattgt gacccggccc ttg	33					
	<210><211><211><212><213>	20						
	<220> <223>	Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of humanized anti-Fas antibody						
	<400	> 162						

